Description

Method of Judging Risk for Onset of Drug-Induced Granulocytopenia

Technical Field

[0001]

The present invention relates to a method for assessing the risk of drug-induced granulocytopenia by use, as an index, of a polymorphism of the human insulin receptor substrate-2 gene; to a method of detecting the genetic polymorphism employed as an index for the aforementioned risk assessment; to oligonucleotides employed for these methods; and to a kit for the assessment and/or the detection.

Background Art

[0002]

The mainstay of modern medicine is drug therapy, which employs drugs for treating or preventing various diseases. Almost all drugs employed in drug therapy (e.g., low-molecular-weight compounds) intrinsically are foreign substances to the human body, and thus administration of such drugs provides therapeutic efficacy, but may cause a variety of side effects. Such side effects often compel the drug therapy to be abandoned. Also, some drugs have encountered a situation where research and development have to be suspended due to severe side effects, although the drugs have been proved to be useful for patients with a certain disease. Moreover, the use of some other drugs is strictly regulated in order to detect the sign of

their side effects by mandatory examinations.

[0003]

According to the statistics published in the United States, the cases of drug-induced side effects account for two millions or more a year, and more than 100 thousand due to such side effects (JAMA, 279, 1200 (1998)). In Japan, 26,545 cases of drug-induced side effects (including redundantly reported cases) were reported, and 1,239 deaths due to such side effects only in one year of 2000 (Ministry of Health, Labor and Welfare, June 6, 2003, House of Representatives, Responsive Pleading No. 55).

[0004]

Among side effects due to drug administration, granulocytopenia is a fatal side effect. Particularly, a decrease in granulocytes tends to lead to an infection, and onset of agranulocytosis involves a very high risk for a serious infectious disease such as pneumonia or sepsis. Examples of drugs that are generally known to induce granulocytopenia include analgesic-antipyretic drugs (aminopyrine), antibiotics (Chloromycetin), antithyroid drugs (Mercazole), anticonvulsant drugs, antidiabetic drugs, and diuretic drugs. Occurrence of side effects caused by such a drug is less likely to be related to its dose, and is considered to be related to the predisposition of a patient (e.g., allergic predisposition or idiosyncrasy). Therefore, occurrence of such side effects is almost impossible to predict. In order to avoid occurrence of such side effects, doctors must handle respective cases very carefully, through detailed interviews with individual patients regarding, for

example, drug administration records in other departments, and analysis of blood test results, etc. Notably, if and when a patient has onset a side effect of granulocytopenia, doctors must take immediate measures, including hospitalization.

[0005]

Other drugs that are known to induce granulocytopenia include dibenzodiazepine (clozapine), which is an antipsychotic drug. This drug is expected to have high efficacy, but clinical trials of the drug have been suspended in Japan.

Other drugs that induce granulocytopenia include vesnarinone, which has inhibitory activities on PDE3 and K channel. This drug is an effective inotropic drug that is less likely to cause arrhythmia and other cardiac events (e.g., onset of heart failure and hospitalization). However, administration of this drug may cause side effects; i.e., leukopenia, granulocytopenia, and subsequent agranulocytosis. Therefore, the use of this drug is strictly limited.

[0006]

Single nucleotide polymorphisms (SNPs) are the most frequently used genetic markers in human genetic analysis. SNPs have already been shown to be useful markers for an association study between genetic background and common diseases or drug response (see Non-Patent Documents 1, 2, and 3). As has been known, analysis of haplotype, constructed of multiple SNPs, is useful for analysis of the susceptibility of polygenic diseases (see Non-Patent Documents 4 and 5). In practice, some diseases such as Alzheimer's disease and hypertension have already been

intensively analyzed by such an analysis method (Jeunemaitre, X., *et al.*, Am. J. Hum. Genet., 60, 1448-1460 (1997); Martin, E. R., Am. J. Hum. Genet., 67, 383-394 (2000)).

[0007]

In recent years, advances in genome analysis have led to development of toxicogenomics, which studies relationship between genes and toxicities such as the effect of a drug on cytochrome P450 (CYP) (i.e., a drug-metabolizing enzyme). Particularly, association studies of individual genetic background and sensitivity/response has been proposed as a powerful tool to elucidate the cause of adverse effects. So-called tailor-made therapy is expected to be realized through these approaches

Non-Patent Document 1: Brookes, A. J., "The essence of SNPs," Gene, USA, (1999), 234, 177-186

Non-Patent Document 2: Cargill, M, *et al.*, "Characterization of single-nucleotide polymorphisms in coding regions of human genes," Nature Genet., USA, (1999), 22, 231-238

Non-Patent Document 3: Evans, W. E., & Relling, M. V., "Pharmacogenomics: translating functional genomics into rational therapeutics," Science, USA, (1999), 286, 487-491

Non-Patent Document 4: Stephens, J. C., *et al.*, "Dating the origin of the CCR5-Delta32 AIDS-resistance allele by the coalescence of haplotypes," Am. J. Hum. Genet., USA, (1998), 62, 1507-1515

Non-Patent Document 5: Tishkoff, S. A., *et al.*, "The accuracy of statistical methods for estimation of haplotype frequencies: an example from the CD4 locus," Am. J. Hum. Genet., USA, (2000), 67,

518-522

Disclosure of the Invention

Problems to be Solved by the Invention

[0008]

A primary object of the present invention is to provide means for assessing the risk of drug-induced granulocytopenia by use, as an index, of polymorphisms of the human insulin receptor substrate-2 gene, or means for detecting the genetic polymorphisms employed as an index for the risk assessment means.

Means for Solving the Problems

[0009]

In order to solve the aforementioned problems, firstly, the present inventors have selected, as genes for polymorphism analysis, 115 candidate genes, including cytokine-related genes, MHC region genes, G-CSF-related genes, TNF-α-related genes, NFκ-related genes, cAMP-related genes, and K-channel-related genes, searched for SNPs in these candidate genes from the database of Japanese Single Nucleotide Polymorphisms, and picked up 188 candidate SNPs for analysis.

[0010]

Subsequently, the present inventors have determined the frequency of these SNPs in the genomic DNA of samples from the following two groups: a group of subjects with granulocytopenia induced by administration of a specific drug, and a group of subjects without granulocytopenia who have received the same drug. As a result, the present inventors have confirmed that SNPs with the most statistically significant difference between the

aforementioned two groups are present on the insulin receptor substrate-2 gene (J-SNP ID: IMS-JST040476) (hereinafter, the gene will be referred to as "the IRS-2 gene").

[0011]

Furthermore, the present inventors have conducted extensive studies on the relationship between polymorphisms in the human IRS-2 gene and drug-induced granulocytopenia, and as a result have confirmed that six SNPs of the human IRS-2 gene are intimately related to granulocytopenia induced by administration of the drug.

The present inventors have found that analysis of these specified SNPs enables assessment (predictive diagnosis) of the risk of side effects induced by drugs for various human diseases; particularly, the risk of onset of drug-induced granulocytopenia. The present invention has been accomplished on the basis of this finding.

[0012]

The present invention provides a method for determining the presence of the risk of drug-induced granulocytopenia, a method of detecting a genetic polymorphism markers employed as an index for the aforementioned risk determination, and oligonucleotides and kit employed for these methods, which are summarized below in (1) through (19).

[0013]

(1) A method for assessing the risk of drug-induced granulocytopenia, the method comprising detecting polymorphisms of the human IRS-2 gene of a subject, and determining the presence

of the risk of drug-induced granulocytopenia of the subject by use of the genetic polymorphisms as an index.

[0014]

(2) A method of detecting polymorphisms of the human IRS-2 gene of a subject for determining the presence of the risk of drug-induced granulocytopenia, in which the genetic polymorphism is employed as an index.

[0015]

(3) An examination method for the risk of drug-induced granulocytopenia, comprising detecting a polymorphism of the human IRS-2 gene of a subject, and carrying out an examination using the genetic polymorphisms as an index for the risk.

[0016]

(4) A method as described in any of (1) through (3) above, wherein the presence of the risk of drug-induced granulocytopenia is determined by use, as an index, of at least one genetic polymorphism selected from the group consisting of human IRS-2 gene polymorphisms described below in (a) through (f):

(a) a polymorphism that is C (wild type) to A conversion at position 4,587 upstream of the translation initiation codon;

(b) a polymorphism that is AT deletion (wild type) at position 2,510 upstream of the translation initiation codon;

(c) a polymorphism that is A (wild type) to C conversion at position 1,164 upstream of the translation initiation codon;

(d) a polymorphism that is A (wild type) to G conversion at position 15,870 downstream from the translation initiation codon;

(e) a polymorphism that is A (wild type) to G conversion at position

29,793 downstream from the translation initiation codon; and (f) a polymorphism that it C deletion(wild type) at position 31,532 downstream from the translation initiation codon.

[0017]

(5) A method as described in any of (1) through (4) above, wherein the genetic polymorphisms is detected through at least one technique selected from the group consisting of direct nucleotide sequencing, allele-specific oligonucleotide (ASO)-dot blot analysis, single nucleotide primer extension assay, PCR-single strand conformation polymorphism (SSCP) analysis, PCR-restriction enzyme fragment length polymorphism (RFLP) analysis, Invader assay, quantitative real-time PCR assay, and genetic polymorphism assay employing a mass spectrometer (mass array).

[0018]

(6) A method as described in (5) above, wherein the genetic polymorphisms is detected through direct nucleotide sequencing.

[0019]

(7) A method as described in (5) above, wherein the genetic polymorphisms are detected through PCR-restriction enzyme fragment length polymorphism (RFLP) analysis.

[0020]

(8) A method as described in (7) above, wherein the PCR-restriction enzyme fragment length polymorphism (RFLP) analysis is performed by use of the restriction enzyme *Afa* I for detecting A to G conversion at position 29,793 downstream from the translation initiation codon of the human IRS-2 gene.

[0021]

(9) An oligonucleotide which can be hybridized with the human IRS-2 gene and is employed as a primer or probe for genetic polymorphism detection, the oligonucleotide being selected from the group consisting of oligonucleotides described below in (a) through (f):

(a) an oligonucleotide having a sequence including a genetic polymorphism that is C to A conversion at position 4,587 upstream of the translation initiation codon of the human IRS-2 gene;

(b) an oligonucleotide having a sequence including a genetic polymorphism that is AT deletion at position 2,510 upstream of the translation initiation codon of the human IRS-2 gene;

(c) an oligonucleotide having a sequence including a genetic polymorphism that is A to C conversion at position 1,164 upstream of the translation initiation codon of the human IRS-2 gene;

(d) an oligonucleotide having a sequence including a genetic polymorphism that is A to G conversion at position 15,870 downstream from the translation initiation codon of the human IRS-2 gene;

(e) an oligonucleotide having a sequence including a genetic polymorphism site that is A to G conversion at position 29,793 downstream from the translation initiation codon of the human IRS-2 gene; and

(f) an oligonucleotide having a sequence including a genetic polymorphism that is C deletion at position 31,532 downstream from the translation initiation codon of the human IRS-2 gene.

[0022]

(10) An oligonucleotide, which can be hybridized with the human IRS-2 gene is employed as a primer for genetic polymorphism detection, the oligonucleotide being selected from the group consisting of oligonucleotides described below in (a) through (d) and (f):

(a) an oligonucleotide having the sequence of SEQ ID NO: 3;

(b) an oligonucleotide having the sequence of SEQ ID NO: 6;

(c) an oligonucleotide having the sequence of SEQ ID NO: 9;

(d) an oligonucleotide having the sequence of SEQ ID NO: 12; and

(f) an oligonucleotide having the sequence of SEQ ID NO: 17.

[0023]

(11) A kit for assessing the risk of drug-induced granulocytopenia, the kit comprising an oligonucleotide as described in (9) above serving as a primer or probe for detecting a polymorphism of the human IRS-2 gene.

[0024]

(12) A kit as described in (11) above, which comprises oligonucleotides as described in (10) above.

[0025]

(13) A kit as described in (11) above, which comprises the oligonucleotide as described in (e) of (9) above and the restriction enzyme *Afa* I, the kit being employed for detecting A to G conversion at position 29,793 downstream from the translation initiation codon of the human IRS-2 gene.

[0026]

(14) A method as described in (1) above, which assesses the risk of drug-induced granulocytopenia attributed to vesnarinone

administration by use of oligonucleotides as described in (9) or (10) above.

[0027]

(15) A method as described in (1) above, which assesses the risk of drug-induced granulocytopenia attributed to vesnarinone administration by use of the oligonucleotides as described in (e) of (9) above and the restriction enzyme *Afa* I.

[0028]

(16) A kit for detecting a polymorphism of the human IRS-2 gene employed for determining the presence of the risk of drug-induced granulocytopenia, the kit comprising oligonucleotides as described in (9) above as primers or probes for detecting the IRS-2 gene polymorphisms.

[0029]

(17) A kit as described in (16) above, which comprises oligonucleotides as described in (10) above.

[0030]

(18) A kit as described in (16) above, which comprises the oligonucleotides as described in (e) of (9) above and the restriction enzyme *Afa* I, the kit being employed for detecting A to G conversion at position 29,793 downstream from the translation initiation codon of the human IRS-2 gene.

[0031]

(19) A method as described in (2) above, which detects a genetic polymorphism employed for assessing the risk of drug-induced granulocytopenia attributed to vesnarinone administration by use of oligonucleotides as described in (9) or

(10) above.

[0032]

(20) A method as described in (2) above, which detects a genetic polymorphism employed for assessing the risk of drug-induced granulocytopenia attributed to vesnarinone administration by use of the oligonucleotides as described in (e) of (9) above and the restriction enzyme *Afa* I.

[0033]

(21) A method as described in (3) above, in which the examination is carried out concerning the risk of drug-induced granulocytopenia attributed to vesnarinone administration, by use of oligonucleotides as described in (9) or (10) above.

[0034]

(22) A method as described in (3) above, in which the examination is carried out concerning the risk of drug-induced granulocytopenia attributed to vesnarinone administration, by use of oligonucleotides as described in (e) of (9) above and the restriction enzyme *Afa* I.

Effects of the Invention

[0035]

According to the present invention, there are provided methods for assessing the risk of drug-induced granulocytopenia in a human; a method of detecting a genetic polymorphism employed as an index for the aforementioned assessment; kits for these methods; primers and probes for polymorphism detection, which are employed in these methods; and a gene relating to a risk factor for drug-induced granulocytopenia in a human. These are useful

for examining or assessing the risk of human drug-induced granulocytopenia, particularly useful for examining or assessing the risk of human drug-induced granulocytopenia before administration of a drug which has already been reported to induce granulocytopenia (including agranulocytosis).

Brief Description of the Drawing

[0036]

[Fig. 1] A schematic representation showing the structure of the human IRS-2 gene and the positions of polymorphisms of the gene.

Best Mode for Carrying Out the Invention

[0037]

As used herein, abbreviations of amino acids, peptides, nucleotide sequences, nucleic acids, etc. are according to IUPAC-IUB nomenclature [IUPAC-IUB communication on Biological Nomenclature, Eur. J. Biochem., 138: 9 (1984)], "Guideline for preparation of a specification, etc. including nucleotide sequences or amino acid sequences" (edited by Japan Patent Office), and commonly employed symbols used in the field.

[0038]

As used herein, the genomic sequence of the human IRS-2 gene is included in the sequence reported by Mohammadi, M. at Sanger Center (GenBank accession No: AL162497), which has a full length of 143,409 bp.

[0039]

The IRS-2 gene, whose structure is estimated by the genomic sequence on the basis of the sequence data of IRS-2 mRNA sequence

obtained from GenBank (accession number XM 007095) and the sequence data of the aforementioned AL162497, is a 32,730bp composed of two exons and one intron. The IRS-2 gene corresponds to 93,673 to 126,402 bp in the sequence of AL162497. Fig. 1 schematically shows the structure of the IRS-2 gene. In Fig. 1, "Ex. 1" and "Ex. 2" correspond to the aforementioned two exons. Abbreviations with arrows correspond to the below-described alterations (SNPs). Notably, the SNPs are synonymous; i.e., the SNPs do not cause amino acid substitutions, and therefore the protein sequence does not be changed. The position numbers of SNPs as described in the specification or the figure correspond to the position numbers counting from A of ATG that is used as a codon for Met at N-terminus of protein when mRNA is translated into protein (translation initiation codon).

C-4587A: C to A conversion at position 4,587 upstream of the translation initiation codon of the human IRS-2 gene;

AT-2510del: AT deletion at position 2,510 upstream of the translation initiation codon of the human IRS-2 gene;

A-1164C: A to C conversion at position 1,164 upstream of the translation initiation codon of the human IRS-2 gene;

A15870G: A to G conversion at position 15,870 downstream from the translation initiation codon of the human IRS-2 gene;

A29793G: A to G conversion at position 29,793 downstream from the translation initiation codon of the human IRS-2 gene; and

C31532del: C deletion at position 31,532 (in Ex. 2) from the translation initiation codon of the human IRS-2 gene.

[0040]

As used herein, the term "gene" encompasses double-stranded DNA, as well as single-stranded DNA (sense strand or antisense strand) constituting the double-stranded DNA. Unless otherwise specified, the gene (DNA) employed in the present invention encompasses double-stranded DNA including human genomic DNA, single-stranded DNA including cDNA (sense strand), single-stranded DNA having a sequence complementary to the sense strand, and fragments thereof. The aforementioned gene (DNA) may include regulatory regions, coding regions, exons, and introns. The term "polynucleotide" encompasses RNA and DNA. The term "DNA" encompasses cDNA, genomic DNA, and synthetic DNA. The term "polypeptide" encompasses its fragments, homologues, derivatives, and mutants. The term "mutant" refers to a naturally occurring allele mutant, a non-naturally occurring mutant, a mutant obtained through alteration (deletion, substitution, addition, or insertion), and a polynucleotide sequence which does substantially not change the function of the polypeptide encoded by the polynucleotide sequence. Alteration of an amino acid sequence, which may naturally occur through, for example, mutation or post-translational modification, can be artificially performed by introducing mutations into the gene.

[0041]

As used herein, the term "SNP (single nucleotide polymorphism)" refers to alteration of a single nucleotide in a gene or gene cluster, and "SNPs" refers to plural form of SNP. The term "haplotype" refers to the type of the aforementioned

single strand marker constructed of multiple polymorphic sites of a continuous gene region or gene cluster.

[0042]

The present invention has been accomplished on the basis of the finding that a polymorphism(s) including alteration at a specific site of the human IRS-2 gene (the entirety of the IRS-2 gene including the promoter region involved in transcriptional regulation), particularly, SNP or SNPs are intimately correlated with human drug-induced granulocytopenia, and the risk of drug-induced granulocytopenia can be assessed (pre-diagnosed) by detecting the SNPs as a genetic polymorphism marker at the specific site. The assessment method of the present invention involves detection of a polymorphism(s) (i.e., SNP or SNPs) of the human IRS-2 gene of a sample (derived from a subject).

[0043]

The SNPs detected and analyzed by the method of the present invention (i.e., genetic alterations serving as an index for assessing the risk of drug-induced granulocytopenia) include the aforementioned six polymorphisms; i.e., C-4587A, AT-2510del, A-1164C, A15870G, A29793G, and C31532del. The positions of the SNPs on the IRS-2 gene are as shown in Fig. 1. Notably, the position numbers of the SNPs correspond to the position numbers counting from A of ATG that is used as a codon for Met at N-terminus of protein when mRNA is translated into protein (translation initiation codon).

[0044]

The present invention enables detection of polymorphisms

(SNPs and haplotype) of the human IRS-2 gene, which provides data or means useful for elucidation and understanding of the mechanism of drug-induced granulocytopenia in human, and for diagnosis and prevention of the disease. According to the present invention, when a subject having the risk of drug-induced granulocytopenia is determined, and administration of a drug to the subject is avoided, drug-induced granulocytopenia can be prevented. Moreover, when other assays are performed frequently in addition to the present invention to monitor side effects upon administration of a drug, effective measures can be taken against such side effects.

[0045]

The method of the present invention will next be described in detail.

In the method of the present invention, polymorphisms of the human IRS-2 gene of a subject are detected, and the presence of the risk of drug-induced granulocytopenia is determined by use of the genetic polymorphisms as an index.

Detection of thepolymorphisms of the human IRS-2 gene is performed through, for example, the following procedure: the genomic sequence of the human IRS-2 gene of a subject, or its complementary strand is prepared, and, if desired, the genomic sequence or the sequence of its complementary strand is determined, followed by detection of the gene polymorphisms.

[0046]

Preparation of human IRS-2 gene including SNPs

The human IRS-2 gene derived from a subject is prepared as

a sample for DNA analysis. Specific examples of the gene having polymorphisms (SNPs) are as described above. The IRS-2 gene encompasses the above-exemplified complementary strand of the DNA sequence of the human IRS-2 gene.

[0047]

The human IRS-2 gene, which has genetic polymorphisms, or its complementary strand can be readily prepared through a generally employed genetic engineering technique on the basis of specific sequence data of the human IRS-2 gene as disclosed herein [see, for example, Molecular Cloning 2nd Ed, Cold Spring Harbor Lab. Press (1989); or *Zoku Seikagaku Jikken Koza "Idenshi Kenkyuho* I, II, III" edited by The Japanese Biochemical Society (1986)].

[0048]

Specifically, cDNA or genomic DNA is extracted, through a common method, from a subject (e.g., a patient with human drug-induced granulocytopenia who has SNPs of the human IRS-2 gene), and a target clone is selected through a common method employing, for example, an appropriate antibody, restriction enzyme, or probe which may include a specific polymorphism of the human IRS-2 gene [see, for example, Proc. Natl. Acad. Sci., U.S.A., 78, 6613 (1981); or Science, 222, 778 (1983)], to thereby prepare a target genomic sequence of the IRS-2 gene.

[0049]

Examples of the source of the aforementioned cDNA or genomic DNA include various cells and tissues having the IRS-2 gene including SNPs, and cultured cells derived therefrom. Other examples of the source include body fluids such as blood (e.g.,

serum or plasma), saliva, lymph, airway mucus, urine, and semen. The aforementioned source material (serving as a sample) is preferably DNA or genomic DNA derived from a human subject before administration of a drug (in particular, a drug which has previously been reported to induce granulocytopenia). Isolation of RNA from such a source material, isolation and purification of mRNA, preparation of cDNA, cloning thereof, etc. can be carried out through a common method. In the present invention, various commercially available cDNA libraries (e.g., cDNA libraries available from Clontech Lab. Inc.) may be employed.

[0050]

No particular limitation is imposed on the method for screening a target gene from cDNA libraries, and the gene screening can be performed through a common method. Specifically, there is a prepared probe including a polymorphic site which can selectively bind to the DNA sequence of target sequence around SNPs, and plaque hybridization, colony hybridization, etc. These methods are performed singly or in combination by use of the thus-prepared probe.

[0051]

The primers employed for screening may be a forward primer or reverse primer designed on the basis of target nucleotide sequence data of the human IRS-2 gene. Such primers can be synthesized through a common method by use of, for example, an automated synthesis apparatus. The probe for screening is generally a labeled probe. However, the screening probe may be an unlabeled probe, so long as it can specifically bind to a

directly or indirectly labeled reagent. The labeling reagent and labeling technique such a probe or ligand have already been well known in the field. Examples of the labeling reagent include radioactive labeling reagents, biotin, fluorescent dyes, chemiluminescent reagents, enzymes (e.g., luciferase), and antibodies, which can be incorporated through a known labeling technique such as nick translation, random priming, or kinase treatment.

[0052]

The thus-extracted genomic DNA or mRNA including the human IRS-2 gene can be amplified through a gene amplification method. This gene amplification enables easier and accurate detection through the detection method of the present invention. Examples of the gene amplification method include PCR (Saiki, R. K., Bugawan, T. L., *et al.*, Nature, 324, 163-166 (1986)), NASBA (Comptom, J., Nature, 650, 91-92 (1991)), TMA (Kacian, D. L., and Fultz, T. J., US Patent No. 5,399,491 (1995)), and SDA (Walker, G. T., Little, M. C., *et al.*, Proc. Natl. Acad. Sci., U.S.A., 89, 392-396 (1992)).

[0053]

Gene fragments amplified by means of, for example, PCR may be isolated and purified through a common technique such as gel electrophoresis. Alternatively, purification of such gene fragments may be performed by use of a column. The gene fragment purification can be confirmed through, for example, mass spectrometry. In accordance with properties of the thus-amplified gene fragments, the gene fragments are applied for

detection of the human IRS-2 gene (SNPs) employed in the present invention.

[0054]

Detection of human IRS-2 gene polymorphism

In the method of the present invention, subsequently, the presence of a polymorphism(s) of the aforementioned sample is detected. Specifically, this detection can be performed through, for example, any of the below-described methods (1) through (8).

[0055]

(1) Direct nucleotide sequencing

Detection of the IRS-2 gene polymorphism(s) can be performed through a direct nucleotide sequencing method, which has conventionally been employed for sequencing of such a gene; for example, the dideoxy method (Sanger, *et al.*, Proc. Natl. Acad. Sci., U.S.A., 74, 5463-5467 (1977)) or the Maxam-Gilbert method [Methods in Enzymology, 65, 499 (1980)]. The genetic polymorphism detection may be performed through a combination of such a direct nucleotide sequencing method and a DNA amplification method (e.g., PCR). Particularly, a combination of such a direct nucleotide sequencing method and PCR or a similar DNA amplification method is preferred, since this combination needs only a small amount of a DNA sample, and enables simple and easy detection with high sensitivity and accuracy.

[0056]

Basically, this preferred method can be performed through, for example, the following procedure: a PCR-amplified gene fragment or a purified product thereof is cloned into a plasmid,

followed by direct nucleotide sequencing through the dideoxy method, the Maxam-Gilbert method, or a similar method. For the sake of convenience, the preferred method can be performed through nucleotide sequencing by use of, for example, a commercially available sequencing kit. Thus, the presence of polymorphisms at the aforementioned specific sites of the human IRS-2 gene can be detected.

[0057]

In the aforementioned method and the below-described methods, no particular limitation is imposed on the PCR-amplified DNA fragment (i.e., sample), so long as the DNA fragment includes at least one of the aforementioned specific sites at which polymorphisms is expected to occur. The DNA fragment generally has a length of about 50 to several thousands of bp, preferably 50 to several hundreds of bp.

[0058]

(2) Allele-specific oligonucleotide dot blot method

Alternatively, detection of the IRS-2 gene polymorphism(s) can be performed through the allele-specific oligonucleotide (ASO)-dot blot method (Conner, B. J., *et al.*, Proc. Natl. Acad. Sci., U.S.A., 80, 278-282 (1983)). This method can be performed through, for example, dot blot analysis in which a PCR-amplified gene fragment by use of a forward primer and reverse primer designed so as to sandwich a target is hybridized with an allele-specific oligonucleotide probe containing SNP site. Thus, the presence of SNP in the gene fragment can be determined.

[0059]

(3) Single nucleotide primer extension assay

Detection of the IRS-2 gene polymorphism(s) can also be performed through a single nucleotide extension assay, such as the SNaPshot assay, pyrosequencing, or the point mutation detection assay disclosed in Japanese Patent Application Laid-Open (*kokai*) No. 2000-279197. In such an assay, a probe designed so as to correspond to a nucleotide immediately (or several nucleotides) before a target polymorphism (SNP) (i.e., a probe designed such that the 3'-end thereof corresponds to one (or several) nucleotide upstream of the polymorphism) is annealed to a DNA sample. Each of the aforementioned assays can be performed by use of a commercially available SNPs detection kit and the software attached to the kit.

[0060]

For example, the SNaPshot assay can be performed by use of ABI PRISM SNaPshot ddNTP Primer Extension Kit (PE Applied Biosystems). Detection of SNPs can be performed through detection and analysis of fluorescent fragments generated after reaction by use of ABI PRISM 310/377/3100/3700 DNA Analyzer (PE Applied Biosystems) and GeneScan software.

[0061]

Pyrosequencing can be performed through, for example, the following procedure. Specifically, genomic DNA is isolated from, for example, a blood sample through a common method; several tens to several hundreds of nucleotides (including a polymorphism) are PCR-amplified by use of a biotin-labeled primer; single-stranded DNA is purified by use of magnet beads; and the thus-purified DNA

is employed as a sample. A primer designed to have a complementary sequence corresponding to several nucleotides upstream of a target polymorphism is annealed to the sample, and then each dNTP is added to the mixture none after another according to the sequence in the vicinity of the polymorphism input in software. Pyrophosphoric acid (PPi) released from nucleotide extension of DNA polymerase is converted to ATP by ATP sulfurylase, and luciferase generates detectable light using this ATP, which can be detected with a chemiluminescence detector, a CCD camera, etc. Thus, genotyping can be performed through analysis of the peak of luminescence obtained through addition of the dNTPs. This method enables genotyping in about 15 minutes for 96 samples. [0062]

The aforementioned method can use a generally employed reagent and apparatus. Examples include reagents such as commercially available SNP Reagent Kits (Pyrosequencing AB) which contain, as components, a mixture of the following four enzymes: DNA polymerase, ATP-sulfurylase, luciferase, and apyrase, a substrate solution containing luciferin and APS (adenosine 5'-phosphosulfate), and dNTPs containing dATP (deoxyadenosine 5'-triphosphate), dCTP, dGTP, and dTTP; PSQ96 system for automatic DNA sequence analysis (Pyrosequencing AB); and SNP software employed for the analysis (Pyrosequencing AB). [0063]

Alternatively, pyrosequencing can be performed through, for example, the method described in US Patent No. 6,159,693. Specifically, an isolated genomic DNA is amplified; the

thus-amplified PCR product is purified; and the resultant product is reacted with pyrophosphoric acid by use of READIT™ System (Promega Corporation), followed by analysis of the resultant data.

[0064]

(4) PCR-single strand conformation polymorphism (SSCP) analysis

The detection method of the present invention can employ the PCR-SSCP method (Orita, M., Iwahara, H., *et al.*, Proc. Natl. Acad. Sci., U.S.A., 86, 2776-2770 (1989)), in which an amplified PCR product (single-stranded DNA) is subjected to non-denatured polyacrylamide gel electrophoresis, and the presence of single nucleotide polymorphims is determined on the basis of the mobility difference.

[0065]

(5) PCR-restriction enzyme fragment length polymorphism (RFLP) analysis

In the present invention, in the case where, for example, a nucleotide sequence including a polymorphims, which are targeted for detection of SNPs or haplotype of the human IRS-2 gene, contains a restriction enzyme recognition site, the detection can be performed through restriction enzyme fragment length polymorphism analysis (RFLP analysis: Botstein, D. R., *et al.*, Am. J. Hum. Gen., 32, 314-331 (1980)).

[0066]

Specifically, for example, there is employed a restriction enzyme which can recognize nucleotides around the polymorphism,

in order to detect whether the nucleotide at position 29,793 is A (wild type) or G (mutant type), the position being counted from the translation initiation codon present in Ex. 2 of the human IRS-2 gene. The enzyme employed in the RFLP analysis may be any known restriction enzyme, so long as the enzyme can recognize nucleotides around thetarget polymorphisms. Specific examples of the restriction enzyme include *Afa* I.

[0067]

The RFLP analysis is more preferably done as PCR-RFLP analysis; i.e., analysis performed on a large amount of sample DNA which has been amplified and prepared in advance through PCR or a modification thereof. Thus, the presence of polymorphism can be detected on the basis of the presence of a specific cleavage site.

[0068]

More specifically, detection of SNP of the human IRS-2 gene by the PCR-RFLP analysis is performed through, for example, the following procedure. Firstly, the genomic DNA of the human IRS-2 gene is extracted from a human biological sample, and a DNA fragment of the region including a polymorphism of the gene is amplified, thereby preparing a large amount of a DNA sample. The forward primer and/or reverse primer to be employed may be a primer whose sequence is not completely identical to the genomic sequence, as long as is a primer containing a sequence for introducing a restriction enzyme recognition site. Subsequently, the above-amplified DNA sample is digested by use of a specific restriction enzyme (i.e., an enzyme which can digest either a wild

type or a mutant type), and DNA cleavage patterns (e.g., the presence of cleavage, or the base length of cleaved fragments) are confirmed through a common method such as gel electrophoresis.

[0069]

In the case of the polymorphism (A29793G) of the human IRS-2 gene specified by the present invention, which is associated with human drug-induced granulocytopenia, a specific recognition site (GTAC) of the restriction enzyme *Afa* I is generated by the SNP in the region including positions 29,793 to 29,796 of the nucleotide sequence of the human IRS-2 gene. Therefore, this polymorphism can be detected through the RFLP analysis.

[0070]

(6) Invader assay

Detection of SNPs of the IRS-2 gene can also be performed through the Invader assay. The Invader assay can be performed with reference to the following publications:

· Lyamichev, V., *et al.*, Nat. Bioltechnol., 17(3) 292-296 (1999); and

· International Patent Publication WO 9823774 (Japanese *Kohyo* Patent Publication No. 2001-526526).

The Invader assay enables analysis of SNPs of genomic DNA without amplification of target DNA. For example, the Invader assay is performed as follows.

[0071]

In order to detect the presence of target SNPs of the human IRS-2 gene, firstly, genomic DNA is isolated. To perform this assay, two oligonucleotides were prepared by use of, for example,

an automated DNA synthesis apparatus. One oligonucleotide, the allele-specific probe, contains the complementary base of the SNP nucleotide to be analyzed, and extends to the upstream of the SNP. Additional non-complementary nucleotides, which are composed of 15 to 50 nucleotides (5' flap), were added to this probe on its 5' site. The second oligonucleotide having 15 to several tens of nucleotides, the Invader oligonucleotide probe, has a complementary sequence to the downstream of the SNP and the end of the probe is a non-matching base overlapping the SNP nucleotide to be analyzed. The two oligonucleotides and an enzyme (i.e., Cleavase for the Invader assay employed in the present invention) are added to the target genomic DNA, which is extracted from described above. This enzyme recognizes the specific structure composed of the two oligonucleotides and the target genomic DNA. This reaction mixture is reacted under the appropriate conditions.

When the genomic DNA of a sample has a target SNP, a first reaction proceeds; the enzyme cleaves the 5' flap. On the other hand, when the genomic DNA of a sample does not have a target SNP, the enzyme does not cleave it.

[0072]

The 5' flap released from the allele-specific probe which has been cleaved by the enzyme is complementarily bound to a fluorescence resonance energy transfer (FRET) probe serving as a target, and the 3'-end of the 5' flap is invaded in the FRET probe. In a manner similar to that described above, enzymatic reaction (second reaction) occurs, and a fluorescent dye is

released.

The FRET probe employed in this second reaction is formed such that it doesn't depend on a target to be detected, and contains the following two essential elements:

(1) a 3' region which is complementary to a product cleaved through the first reaction; and

(2) a self-complementary region which forms a duplex for mimicking a single-stranded probe, which is hybridized with a target, and which contains a reporter fluorescent dye and a quencher fluorescent dye.

[0073]

When the reporter fluorescent dye and the quencher fluorescent dye are bound to the same probe, the fluorescence intensity of the reporter fluorescent dye is quenched through fluorescence resonance energy transfer. Whereas when the reporter fluorescent dye and the quencher fluorescent dye are not bound to the same probe, the fluorescence intensity of the reporter fluorescent dye is not quenched. When the 5' flap released from the cleaved first probe is hybridized with the FRET probe, the resultant product acts as an invader oligonucleotide in the second reaction, and an invasion complex that is recognized by the enzyme is produced. Thus, cleavage of the FRET probe by the aforementioned enzyme separates the two fluorescent dyes, thereby yielding a detectable fluorescent signal. The signal can be read by use of, for example, a standard fluorescence microtiter plate reader, whereby the presence of target SNPs can be detected. A combination of the first and second reactions can amplify the

signal by a factor of 1×10^6. Employment of two FRET probes having different fluorescent dyes also enables detection of the presence of SNP.

[0074]

(7) Quantitative real-time PCR assay

Detection of polymorphisms of the human IRS-2 gene can also be readily performed by quantitative real-time PCR assay (TaqMan assay).

This assay can be performed through, for example, the following procedure. Specifically, firstly, to confirm the presence of a polymorphism, a DNA fragment is prepared as a forward primer or reverse primer formed of, for example, 15 to 39 nucleotides. In this case, the forward primer or reverse primer is prepared so as not to contain the polymorphims. Subsequently, there is prepared a probe which has both a reporter fluorescent dye and a quencher fluorescent dye, and the probe contains, for example, a 15 to 50 bp oligonucleotide which correspond to a partial sequence of amplified fragment. The nucleotide sequence of the probe has to be selected such that a region with which both of the forward and reverse primer do not hybridize. The probe is designed so as to have a sequence complementary to an allele-specific sequence for detecting the presence of a target single nucleotide polymorphism. By use of the probe, a target DNA fragment of the IRS-2 gene of a sample to be detected is amplified through PCR, and fluorescence from the resultant reaction mixture is real-time measured. Thus, the presence of polymorphism can be detected. Employment of two probes having

different fluorescent dyes also enables detection of both alleles.

[0075]

The reporter fluorescent dye employed in the aforementioned Invader assay or TaqMan assay is preferably a fluorescein fluorescent dye such as FAM (6-carboxy-fluorescein), whereas the quencher fluorescent dye is preferably a rhodamine fluorescent dye such as TAMRA (6-carboxy-tetramethyl-rhodamine). These fluorescent dyes are known, and are contained in commercially available real-time PCR detection kits. In the present invention, such a commercially available fluorescent dye can be employed. No particular limitation is imposed on the binding position of the reporter fluorescent dye or the quencher fluorescent dye, but generally, the reporter fluorescent dye is bound to one end (preferably the 5'-end) of the oligonucleotide constituting the probe, and the quencher fluorescent dye is bound to the other end. The method for binding a fluorescent dye to an oligonucleotide is known, and is described in, for example, Noble, *et al.*, (1984), Nuc. Acids Res., 12: 3387-3403 or Iyer, *et al.*, (1990), J. Am. Chem. Soc., 112: 1253-1254.

[0076]

The TaqMan assay *per se* is known, and apparatuses and kits for the TaqMan assay are commercially available. In the present invention, such a commercially available apparatus or kit can be employed. For example, the TaqMan assay can be performed according to the method described in Japanese Patent No. 2,825,976, or according to the ABI PRISM 7700 sequencing system user manual

(PE Applied Biosystems).

[0077]

(8) Genetic polymorphism assay employing a mass spectrometer (mass array)

The mass array assay detects the difference in molecular weight between polymorphisms. Specifically, a region including a polymorphism to be detected is amplified through PCR, and then an extension primer is hybridized with a sequence immediately before the position of SNP, followed by extension reaction by use of a reaction mixture containing a ddNTP/dNTP mixture (e.g., a reaction mixture containing ddATP, dCTP, dGTP, and dTTP), thereby yielding a fragment having a length depending on the type of SNP. The resultant fragment is purified, and then subjected to analysis by use of, for example, a MALDI-TOF mass spectrometer, whereby the relationship between the molecular weight and the genetic polymorphism can be analyzed (Pusch, W., Wurmbach, JH., Thiele, H., Kostrzewa, M., MALDI-TOF mass spectrometry-based SNP genotyping, Pharmacogenomics, 3 (4): 537-48 (2002)). This assay can be readily performed by use of, for example, Sequenom Mass ARRAY high throughput SNP analysis system (http://www.sequenom.com/Files/applications/hme_assay.html).

[0078]

(9) Other detection methods

Detection of SNPs of the human IRS-2 gene can also be performed through, for example, any of the below-described various methods, which have conventionally been known as DNA sequencing methods or mutation detection methods.

(a) PCR-SSO method employing sequence-specific oligonucleotide

A method in which a probe for a mutation is immobilized on a carrier; a sample (gene amplified product) is hybridized with the probe; and a difference in hybridization efficiency is determined on the basis of the presence of mismatch.

(b) PCR-SSP method for point mutation detection

A method by use of a sequence-specific primer for gene amplification which is designed such that a nucleotide corresponding to point mutation becomes the 3'-end nucleotide, which method utilizes that a significant difference in PCR amplification efficiency occurs depending on the complementarity of the 3'-end nucleotide of the primer.

(c) PCR-DGGE (denaturing gradient gel electrophoresis)

When DNA fragment including a mutation is hybridized with a normal DNA fragment, and then the thus-hybridized product is electrophoresed on a polyacrylamide gel with gradually increasing denaturant (e.g., urea or formamide) concentrations, the product is converted into single-stranded DNA fragments at a position of lower denaturant concentration, as compared with the case of non-mismatched homogenous double-stranded DNA fragments. The single-stranded DNA fragments migrate at a rate higher than the migration rate of the double-stranded DNA fragments, and therefore single nucleotide mutation can be detected through comparison of the mobilities of the DNA fragments.

(d) PCR-DGGE/GC clamp method (Shefield, V. C., *et al.*, Proc. Natl. Acad. Sci., U.S.A., 86, 232-236 (1989))

This method is a modification of the aforementioned PCR-DGGE, in which a region having a high GC content is added to a target DNA fragment for detection of a mutation. This method compensates for the disadvantage of the PCR-DGGE in detection of substitution, deletion, addition, or insertion of multiple nucleotides. This method requires a step of adding a GC clamp to a target DNA fragment for mutation detection.

(e) RNase protection assay (Finkelstein, J., *et al.*, Genomics, 7, 167-172 (1990))

(f) In situ RT-PCR (Nucl. Acids Res., 21, 3159-3166 (1993))

(g) In situ hybridization

(h) Southern blotting (Sambrook, J., *et al.*, Molecular Cloning a Laboratory Manual., Cold Spring Harbor Laboratory Press: NY. (1989))

(i) Dot hybridization assay (see, for example, Southern, E. M., J. Mol. Biol., 98: 503-517 (1975))

(j) Fluorescence in situ hybridization (FISH: Takahashi, E., *et al.*, Hum. Genet., 86, 1416 (1990))

(k) Comparative genomic hybridization (CGH: Kallioneimi, A., *et al.*, Science, 258, 818—821 (1992)), (Spectral karyotyping: SKY: Rowley, J. D., *et al.*, Blood, 93, 2038-2042 (1999))

(l) Method employing yeast artificial chromosome (YAC) vector clone as a probe (Lengauer, C., *et al.*, Cancer Res., 52, 2590-2596 (1992)).

Thus, polymorphisms (SNPs) or haplotype of the human IRS-2 gene can be detected.

[0079]

According to the present invention, when a test sample is confirmed to have a polymorphism(s) of the human IRS-2 gene through detection procedures described above, the sample is judged as a subject with a high risk of drug-induced granulocytopenia.

[0080]

Thus, before administration of a drug, it is determined whether the subject has a high risk of drug-induced granulocytopenia. Therefore, granulocytopenia, attributed to drug administration or other causes, will be prevented by this test.

[0081]

Particularly, detection of SNPs of the human IRS-2 gene according to the present invention is effective in detecting the presence of a risk factor for drug-induced granulocytopenia in a human. That is, screening of the SNPs enables detection of a risk factor for human drug-induced granulocytopenia.

Thus, the present invention provides a method of detecting a polymorphism(s) of the human IRS-2 gene of a subject who may develop drug-induced granulocytopenia. That is, the genetic polymorphism(s) of the human IRS-2 gene can be used as an index to detect a subject who develops drug-induced granulocytopenia.

[0082]

Oligonucleotide

The present invention also provides an oligonucleotide serving as a primer or probe for genetic polymorphism detection, which is used in the assessment (detection) method of the present

invention employing PCR. No particular limitation is imposed on the oligonucleotide, so long as it can specifically amplify a specific region including polymorphisms (SNPs) of the human IRS-2 gene. The oligonucleotide can be appropriately constructed on the basis of sequence data of the human IRS-2 gene and synthesized through common methods.

[0083]

More specifically, the oligonucleotide can be synthesized through a generally employed chemical synthesis method such as the phosphoroamidite method or the phosphotriester method, or can be synthesized by use of a commercially available automated oligonucleotide synthesis apparatus such as Pharmacia LKB Gene Assembler Plus (product of Pharmacia). A double-stranded fragment can be obtained by annealing of a chemically synthesized single-stranded oligonucleotide and its complementary strand under appropriate conditions, or synthesized by using an appropriate primer and DNA polymerase. .

[0084]

Preferred examples of the aforementioned oligonucleotide serving as a probe or primer include partial oligonucleotides corresponding to a DNA fragment designed so as to contain a polymorphism of the human IRS-2 gene. These oligonucleotides have at least a sequence of 10 bases (generally about 10 to 35 a sequence of bases). The oligonucleotide serving as a primer pair may be oligonucleotides having two sequences which are designed and synthesized so as to sandwich SNP of the human IRS-2 gene (genomic sequence). The oligonucleotide serving as a probe may be its

positive clone *per se*.

[0085]

Preferred examples of the aforementioned oligonucleotide serving as a probe or primer include partial sequences corresponding to a DNA fragment designed so as to contain at least one of the following polymorphisms: C to A conversion at position 4,587 upstream of the translation initiation codon of the human IRS-2 gene (C-4587A); AT deletion at position 2,510 upstream of the translation initiation codon of the human IRS-2 gene (AT-2510del); A to C conversion at position 1,164 upstream of the translation initiation codon of the human IRS-2 gene (A-1164C); A to G conversion at position 15,870 from the translation initiation codon of the human IRS-2 gene (A15870G); A to G conversion at position 29,793 downstream from the translation initiation codon of the human IRS-2 gene (A29793G); and C deletion at position 31,532 downstream from the translation initiation codon of the human IRS-2 gene (C31532del). These primer or probe has at least a sequence of 10 basess (preferably at least a sequence of 15 bases).

[0086]

Specific examples of the oligonucleotide include forward primers and reverse primers of SEQ ID NOs: 1, 2, 4, 5, 7, 8, 10, 11 and 13 to 16, and oligonucleotide primers for direct sequencing of SEQ ID NOs: 3, 6, 9, 12, and 17, which are described below in Examples.

[0087]

No particular limitation is imposed on the gene-specific

probe employed in the present invention, so long as it can detect any of the aforementioned C-4587A, AT-2510del, A-1164C, A15870G, A29793G, and C31532del.

[0088]

Kit for assessment

The assessment (detection) method of the present invention can be more easily performed by use of a reagent kit for detecting SNPs of the human IRS-2 gene of a sample. The present invention also provides a kit for such assessment.

[0089]

A kit of the present invention includes, as an essential component, at least a DNA fragment which hybridizes with a partial or entire - nucleotide sequences or its complementary sequences - including six SNPs of the human IRS-2 gene, or which hybridizes with a sequence containing an ologonucleotide with one base or several bases before a polymorphic site. Another kit of the present invention includes, as an essential component, a restriction enzyme (e.g., *Afa* I) that specifically recognizes a sequence formed of several nucleotides (including the aforementioned polymorphic site).

[0090]

Other components of the kit of the present invention are, for example, a labeling reagent, and reagents required for PCR (e.g., Taq DNA polymerase, deoxynucleotide triphosphate, or a primer for DNA amplification). Examples of the labeling reagent include chemical modification substances such as a radioactive isotope, a light-emitting substance, and a fluorescent substance.

The DNA fragment *per se* may be conjugated in advance with such a labeling reagent. The kit of the present invention may further include, for example, - appropriate reaction diluents, standard antibodies, buffers, detergents, or reaction stopping solutions, to perform measurement conveniently.

[0091]

Use of the aforementioned assessment method of the present invention enables provision of an examination method for the risk of human drug-induced granulocytopenia by use, as an index, of a detected genetic polymorphism which may cause drug-induced granulocytopenia in a human, particularly, an examination method for the risk of granulocytopenia attributed to administration of a drug (e.g., vesnarinone) which has already been reported to induce granulocytopenia (including agranulocytosis), before administration of the drug, as well as a diagnosis reagent and diagnosis kit employed for such an examination method.

[0092]

The present invention will next be described in more detail by way of Examples, which should not be construed as limiting the invention thereto.

Example 1

[0093]

Example 1

(a) Screening of genetic polymorphism in relation to granulocytopenia attributed to drug administration

In order to find genetic polymorphisms in relation to granulocytopenia attributed to drug administration, there were

employed subjects who had received vesnarinone (3,4-dihydro-6-[4-(3,4-dimethoxybenzoyl)-1-piperazinyl]-2(1H)-quinoline).

In Japan, vesnarinone, which is a commercially available drug applicable to chronic heart failure (mild to moderate heart failure), has been reported to induce side effects including leukopenia, granulocytopenia, and agranulocytosis, and therefore, administration of this drug requires observation of such side effects and frequent examinations of granulocytes.

Among subjects who had received vesnarinone, had orally agreed to cooperate with investigation of the cause for vesnarinone-induced granulocytopenia between May 1991 and October 1996, and had accepted to provide a blood sample, there were employed 84 subjects (male/female ratio = 1.21 : 1) who had again agreed in writing to cooperate with genetic analysis according to ethical guidelines between July 2001 and December 2001. Genomic DNA was extracted from a blood sample (or a cell sample derived therefrom) of each of the subjects who had again agreed described above. through a common method, and was employed for the below-described tests.

[0094]

(b) Classification criteria of the subjects

On the basis of the below-described criteria, the subjects were classified into the following two groups: a group of subjects with granulocytopenia, and a group of subjects without granulocytopenia.

Among the subjects, subjects having leukocytes or

neutrophils which were decreased to half or less following vesnarinone administration, and having the number of leukocytes of 2,000/mm^3 or less, or the number of neutrophils of 1,000/mm^3 or less were classified as "subjects with granulocytopenia ". On the other hand, subjects who did not decrease the number of neutrophils after vesnarinone administration for 90 days or more were classified as "subjects with granulocytopenia".

Each of these groups was further classified into two groups according to sex, to thereby become four subgroups; i.e., a group of 13 male with granulocytopenia(group A), a group of 17 female with granulocytopenia (group B), a group of 33 male without granulocytopenia (group C), and a group of 21 female without granulocytopenia (group D).

[0095]

(c) Gene and polymorphism (SNP) to be analyzed

115 Candidate genes were selected from among, for example, cytokine-related genes, MHC region genes, G-CSF-related genes, TNF-α-related genes, NF-κ-related genes, cAMP-related genes, and potassium channel-related genes.

Polymorphisms (SNPs) of these candidate genes were searched from the database of Japanese Single Nucleotide Polymorphisms (JSNP: http://snp.ims.u-tokyo.ac.jp/index_ja.html), and 188 candidate SNPs were selected.

[0096]

(d) Analysis method

The SNPs were analyzed by the Invader assay. The Invader assay was performed with reference to the following publications

(1) and (2):

(1) Lyamichev, V., *et al.*, Nat. Biotechnol., 17: 292-296 (1999); and

(2) International Patent Publication WO 9823774 (98/6/4).

In order to amplify genomic DNA regions including each of the candidate SNPs by PCR, a set of primers for amplifying these regions was designed on the basis of genomic DNA sequence data around the SNPs searched from JSNP, and each of the primers was synthesized.

An Invader assay reagent for determining genotypes of the candidate SNPs was prepared by a common method on the basis of genomic DNA sequence data around the SNPs searched from JSNP.

Each PCR was performed by use of genomic DNA (1 ng) as a template. A reaction mixture (15 μL) contained dNTPs (0.25 mM), the PCR buffer attached to TaKaRa Ex Taq (Takara) (1/10 of the total amount for reaction), a set of a forward and a reverse primer (130 nM each), and TaKaRa Ex Taq (Takara) (0.5 U). Each sample was amplified in DNA Engine PTC-0200 (MJ Research). The PCR was performed for 94°C for 2 minutes; then 50 cycles of 94°C for 30 seconds, 56°C (or 58°C or 60°C) for 30 seconds, and 72°C for 90 seconds.

Invader assay reaction was carried out mixing the Invader assay reagent with the PCR product that was diluted with a range of 10 to 1,000-fold. A reaction mixture (15 μL) contained 5.5 × Invader buffer (2.75 μL), 10 × Bioplex FRET Probe Mix (0.75 μL), Cleavase VIII enzyme (200 ng/μL) (1 μL), PPI Mix (3 μL), and the diluted PCR product described above (7.5 μL). . The reaction was

performed at 62°C for 60 to 120 minutes.

[0097]

(e) Genotype determination method

Genotype of each subject was determined based on the intensities of two different fluorescent materials detected as a result of the Invader assay reaction. Thus, the genotypes of the 188 SNPs located in the 115 genes of each subject were determined by the Invader assay.

[0098]

(f) Statistical analysis method

The allele frequencies in the group of subjects with granulocytopenia were compared to that of subjects without granulocytopenia by the contingency χ square test. The odds ratio was estimated through the Brown method (Brown, C. C., Am. J. Epidemiol., 113: 474-480 (1981)). The 95% confidence interval of odds ratio was calculated through the Woolf method.

[0099]

(g) Results

The results of analysis of the 188 SNPs in the 115 genes through the aforementioned method revealed that polymorphism with the most statistically significant assosiation was located in the insulin receptor substrate 2 (IRS-2) gene (JSNP ID: IMS-JST040476). In these subjects, this SNP was in Hardy-Weinberg equilibrium.

The result suggests that the SNP in the human IRS-2 gene is intimately related to the granulocytopeniaattributed to vesnarinone administration, and that the human IRS-2 gene is

likely to play an important role in the pathogenesis of granulocytopenia.

The Human IRS-2 protein (translation product of the human IRS-2 gene) belongs to the insulin receptor substrate protein family (IRSs: IRS-1, IRS-2, IRS-3, and IRS-4). IRSs are activated by insulin receptor tyrosine kinase that phosphorylates tyrosine residues of IRSs. As has been known, Phosphorylated-IRSs are related to the insulin action that is to promote glucose uptake by accelerating translocation of glucose transporter 4 (GLUT-4) from cytoplasm to cell membrane via PI-3 kinase activated by phosphorylated-IRSs. In order to conduct further studies on the relation between the human IRS-2 gene and vesnarinone-induced granulocytopenia, another polymorphisms of the human IRS-2 gene were analyzed.

[0100]

Example 2 Association analysis of the human IRS-2 gene and drug-induced granulocytopenia

By use of the subjects described in Example 1, polymorphisms of the human IRS-2 gene were analyzed as follows.

(a) Discovery of polymorphisms in the Human IRS-2 gene

In order to screen the entirety of the IRS-2 gene including a promoter region involved in its transcriptional regulation, the genomic sequence including the IRS-2 gene was obtained from GenBank (accession number AL162497, full length: 143,409 bp) by inquiring the human IRS-2 mRNA sequence, which is registered in GenBank (accession number XM_007095). The structure of the human IRS-2 gene was estimated through detailed comparison between the

human IRS-2 mRNA sequence and the genomic sequence including the IRS-2 gene. Notably, a complementary strand of the above-obtained genomic sequence was employed for the comparison such that the above-compared sequences were in the same direction (from 5′ to 3′).

It is inferred from the result that the human IRS-2 gene has a full length of 32,730bp including two exons and one intron.

On the basis of the above sequence data, primers were designed and synthesized.

For discovery of polumorphism, there were employed genomic samples from 12 subjects with granulocytopenia and 12 subjects without granulocytopenia among the subjects described in Example 1.

[0101]

Each PCR was performed by use of genomic DNA (5 ng). A reaction mixture (10 μL) was prepared to contain dNTPs (1.25 mM), magnesium chloride (3.9 mM), ammonium sulfate (16.6 mM), Tris-HCl (67 mM, pH 8.8), β-mercaptoethanol (10 mM), a set of a forward primer and a reverse primer (1.25 mM), and TaKaRa Ex Taq (Takara) (0.5 U). If desired, DMSO (dimethyl sulfoxide) was added to the reaction mixture such that the final concentration was 10%.

Each sample was amplified by use of DNA Engine PTC-0200 (MJ Research) or GeneAmp PCR System 9700 (PE Applied Biosystems). The PCR was performed at 95°C for 2 minutes; then 37 cycles of 94°C for 30 seconds, 56°C (or 58°C) for 30 seconds, and 72°C for 3 minutes with final extension at 72°C for 7 minutes.

[0102]

Each of the PCR product was employed to react with BigDye™ Terminator RR mix (PE Applied Biosystems).

On the basis of nucleotide sequence data obtained by ABI Prism 3700 DNA Analyzer (PE Applied Biosystems), genetic polymorphisms were detected and their positions on the human IRS-2 gene were confirmed by use of SEQUENCHER 3.1 (product of Gene Codes)

[0103]

(b) Sample amplification and genotype determination method

In order to determine the genotype distribution, all polymorphisms identified by the discovery above were analyzed in the all subjects described in Example 1 by amplifying the regions containing the polymorphisms with primer sets and sequencing the PCR products under the condition described above.

[0104]

(c) Statistical analysis

In addition to the statistical methods employed in Example 1, a pair-wise linkage disequilibrium coefficient (D' = D/Dmax or D/Dmin) was calculated by use of the method by Thompson, *et al.* (Thompson, E. A., *et al.*, Am. J. Hum. Genet. 42: 113-124 (1988))

[0105]

(d) Results

The analysis results revealed that, in the subject groups, all the polymorphisms analyzed in the present Example are inHardy-Weinberg equilibrium.

The analysis results also revealed that six polymorphisms were intimately associated with granulocytopenia induced by

vesnarinone administration. Tables 1 through 6 show the results of statistical analysis on the six polymorphisms respectively.

[0106]

[Table 1]

Polymorphism The number of genotype	subjects with agranulocytosis N (%)	subjects without agranulocytosis N (%)	χ^2 (df = 1)	P	OR (95% CI)
C-4587A					
CC	7 (25.0)	29 (59.2)	8.36	0.0038	4.35
CA+AA	21 (75.0)	20 (40.8)			(1.56 - 12.16)
Total	28	49			

[0107]

[Table 2]

Polymorphism The number of genotype	subjects with agranulocytosis N (%)	subjects without agranulocytosis N (%)	χ^2 (df = 1)	P	OR (95% CI)
AT-2510del					
AT	7 (24.1)	28 (57.1)	8.02	0.0046	4.19
ATdel+del	22 (75.9)	21 (42.9)			(1.51 - 11.64)
Total	29	49			

[0108]

[Table 3]

Polymorphism The number of genotype	- subjects with agranulocytosis N (%)	- subjects without agranulocytosis N (%)	χ^2 (df = 1)	P	OR (95% CI)
A-1164C					
AA	8 (26.7)	29 (59.2)	7.90	0.0049	3.99 (1.48 - 10.73)
AC+CC	22 (73.3)	20 (40.8)			
Total	30	49			

[0109]

[Table 4]

Polymorphism The number of genotype	subjects with agranulocytosis N (%)	subjects without agranulocytosis N (%)	χ^2 (df = 1)	P	OR (95% CI)
A15870G					
AA	10 (37.0)	36 (73.5)	9.67	0.0019	4.71 (1.72 - 12.88)
AG+GG	17 (63.0)	13 (26.5)			
Total	27	49			

[0110]

[Table 5]

Polymorphism The number of genotype	subjects with agranulocytosis N (%)	subjects without agranulocytosis N (%)	χ^2 (df = 1)	P	OR (95% CI)
A29793G					
AA	11 (36.7)	39 (73.6)	10.90	0.00096	4.81 (1.84 - 12.56)
AG+GG	19 (63.3)	14 (26.4)			
Total	30	53			

[0111]

[Table 6]

Polymorphism The number of genotype	subjects with agranulocytosis N (%)	subjects without agranulocytosis N (%)	χ^2 (df = 1)	P	OR (95% Cl)
C31532del					
CC	9 (33.3)	34 (70.8)	9.93	0.0016	4.86 (1.76 - 13.39)
Cdel+del	18 (66.7)	14 (29.2)			
Total	27	48			

[0112]

In the Tables, a polymorphism with the symbol "del" corresponds to a deletion polymorphism, and the position number of each "polymorphism" correspond to the position number counting from A (position number: +1) of ATG (translation initiation codon) of the IRS-2 gene. A polymorphism shown by the position number with the symbol "-" is located 5' upstream of A of ATG (translation initiation codon) of the IRS-2 gene.

[0113]

As shown in Tables 1 through 6, a subject having at least one of these six polymorphisms has showed association with the granulocytopenia by vesnarinone administration. In other words, these results suggest that one of these polymorphisms, "C-4587A", which is a polymorphism obtained through C to A conversion at position 4,587 upstream of the translation initiation codon of the human IRS-2 gene; "AT-2510del", which is a polymorphism obtained through AT deletion at position 2,510 upstream of the translation initiation codon of the coding region; "A-1164C",

which is a polymorphism obtained through A to C conversion at position 1,164 upstream of the translation initiation codon of the coding region; "A15870G", which is a polymorphism obtained through A to G conversion at position 15,870 downstream from the translation initiation codon of the coding region; "A29793G", which is a polymorphism obtained through A to G conversion at position 29,793 downstream from the translation initiation codon of the coding region; and "C31532del", which is a polymorphism obtained through C deletion at position 31,532 downstream from the translation initiation codon of the coding region, is associated with granulocytopenia by vesnarinone administration. Fig. 1 shows the positions of these six polymorphisms in the human IRS-2 gene. In Fig. 1, "+1" corresponds to A of ATG (translation initiation codon).

Table 7 shows the results of analysis of linkage disequilibrium between these polymorphisms.

[0114]

[Table 7]

SNP	D'				
	C-4587A	AT-2510del	A-1164C	A15870G	A29793G
AT-2510del	1.000	-	-	-	-
A-1164C	1.000	1.000	-	-	-
A15870G	1.000	1.000	1.000	-	-
A29793G	0.956	0.956	0.957	1.000	-
C31532del	0.952	0.953	0.953	1.000	1.000

[0115]

As is clear from Table 7, all the polymorphisms, which are

intimately associated with granulocytopeniaby vesnarinone administration, are in almost complete linkage disequilibrium. Specifically, when the allele at position 4587 upstream of the translation initiation codon of the human IRS-2 gene is A (mutant type), each of the polymorphisms at the other five polymorphic sites has the genotype which shows association with granulocytopeniaby vesnarinone administration.

The results strongly suggest that these six polymorphisms of the human IRS-2 gene play an important role in the granulocytopenia by vesnarinone administration.

[0116]

Recently, it has beenreported that when HL-60 cells (myeloblasts) are differentiated into granulocytes by DMSO stimulation, the amount of IRS-2 protein is increased (Schacher, D. H., *et al.*, J. Immunol., 164: 113-120 (2000)). This report suggests that IRS-2 is closely associated with granulocytic differentiation. Among the human IRS-2 gene polymorphisms analyzed or identified by the present inventors, three polymorphisms (C-4587A, AT-2510del, and A-1164C) are located in the promoter region, which regulates the transcription of the human IRS-2 gene. Therefore, it may be supported that the transcriptional levels of IRS-2 gene are reduced by these polymorphisms located in the promoter region, whereby a differentiation into granulocytes is also reduced..

[0117]

Example 3

This Example is related to other methods for detecting the

six polymorphisms of the human IRS-2 gene of the present invention. In this Example, these polymorphisms were detected through the below-described methods (a) and (b).

(a) Direct sequencing

DNA fragments were amplified by use of forward primers (SEQ ID NOs: 1, 4, 7, 10, 13, and 15) and reverse primers (SEQ ID NOs: 2, 5, 8, 11, 14, and 16) described in Table 8, such that these amplified PCR products included the six polymorphisms according to the present invention. This operation was performed by DNA Engine PTC-0200 (MJ Research) or GeneAmp PCR System 9700 (PE Applied Biosystems) Each PCR was performed for 95°C for 2 minutes; then 37 cycles of 94°C for 30 seconds, the annealing temperature shown in Table 8 for 30 seconds, extension reaction at 72°C for the time shown in Table 8 with final extension at 72°C for 10 minutes. For each of the DNA fragments, as described in Table 8, the annealing temperature and the extension reaction time are 58°C to 60°C and 0.5 minutes to 3 minutes, respectively.

[0118]

[Table 8]

	Forward primer	Nucleotide position number in AL162497	Reverse primer	Nucleotide position number in AL162497	Annealing temperature (°C)	Extension time (min)	DMSO
C-4587A	SEQ ID NO: 1	131420-131399	SEQ ID NO: 2	130318-130339	60	3	-
AT-2510del	SEQ ID NO: 4	128930-128911	SEQ ID NO: 5	127491-127510	60	3	-
A-1164C	SEQ ID NO: 7	127837-127818	SEQ ID NO: 8	126460-126479	60	3	+
A15870G	SEQ ID NO: 10	110260-110240	SEQ ID NO: 11	109859-109879	60	3	-
A29793G	SEQ ID NO: 13	96209-96190	SEQ ID NO: 14	96070-96091	58	0.5	-
C31532del	SEQ ID NO: 15	94616-94595	SEQ ID NO: 16	93139-93159	60	3	-

[0119]

The component of a reaction mixture is as described in Example 2-(a). Notably, DMSO was added to the reaction mixture for detecting "A-1164C" such that the finalconcentration was 10% (see the column "DMSO" of Table 8).

G at position 23 of the reverse primer (SEQ ID NO: 14) employed for detection of "A29793G" described in Table 8 was a replaced base to create the polymorphic site that is recognized by the restriction enzyme *Afa* I.

[0120]

The polymorphisms other than "A29793G" were detected by direct sequencing [the dideoxy method (Sanger, *et al.*, Proc. Natl. Acad. Sci., U.S.A., 74, 5463-5467 (1977) or the Maxam-Gilbert method (Methods in Enzymology, 65, 499 (1980). Table 9 shows primers to determine genotype of each polymorphism (SEQ ID NOs: 3, 6, 9, 12, and 17).

[0121]

[Table 9]

	Primer for sequencing	Nucleotide position number in AL162497
C-4587A	SEQ ID NO: 3	130343-130363
AT-2510del	SEQ ID NO: 6	128581-128562
A-1164C	SEQ ID NO: 9	126912-126929
A15870G	SEQ ID NO: 12	110249-110231
C31532del	SEQ ID NO: 17	94556-94537

[0122]

(b) PCR-RFLP (restriction enzyme fragment length polymorphism) analysis

"PCR-RFLP (restriction enzyme fragment length

polymorphism) analysis was performed to detect "A29793G". Specifically, a reaction mixture (20 μL) contained the PCR product (10 μL), 2 units of restriction enzyme *Afa* I (10 units/mL, Takara), and 10 × Buffer T attached to the restriction enzyme (2 μL). BSA was added to the reaction mixture such that the final concentration was 0.01%, and the resultant mixture was incubated at 37°C for 16 hours. Digested DNA fragments were separated by use of 4% agarose gel and visualized by ethidium bromide staining and ultraviolet transillumination.

[0123]

When DNA extracted from a subject sample is applied to any of the detection methods for the six polymorphisms of the human IRS-2 gene described above in the Examples before administration of a drugwhich may induce granulocytopenia, there can be determined the possibility of an drug-induced granulocytopenia (including agranulocytosis); i.e., the risk of drug-induced granulocytopenia. Thus, according to the present invention, the risk of granulocytopenia attributed to vesnarinone administration can be examined or assessed by of the analysis of DNA from a subject.

Industrial Applicability

[0124]

The present invention is useful for examining or assessing the risk of human drug-induced granulocytopenia, particularly useful for examining or assessing the risk of human drug-induced granulocytopenia before administration of a drug that has already been reported to induce granulocytopenia (including

agranulocytosis).